



#8

SEQUENCE LISTING

<110> GLUCKSMANN, MARIA ALEXANDRA

<120> 93870, A HUMAN G-PROTEIN COUPLED
RECEPTOR AND USES THEREFOR

<130> MPI2001-021P1RCP1M

<140> 10/085,233

<141> 2002-02-28

<150> 60/272,677

<151> 2001-03-01

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1684

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (147)...(1085)

<223> n at position 1384 can be any
nucleotide

<400> 1

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tggaagttgt agactggata agagatgctc agctaaggga gttcctggat ggcctttaga 120
ttgatacacc aatcctctga aattgc atg caa aaa tgt gac ttc cca agt atg 173
                               Met Gln Lys Cys Asp Phe Pro Ser Met
                               1           5
```

```
cct ggc cac aat acc tcc agg aat tcc tct tgc gat cct ata gtg aca 221
Pro Gly His Asn Thr Ser Arg Asn Ser Ser Cys Asp Pro Ile Val Thr
10           15           20           25
```

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ccc cac tta atc agc ctc tac ttc ata gtg ctt att ggc ggg ctg gtg 269
Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu Ile Gly Gly Leu Val
30           35           40
```

```
ggt gtc att tcc att ctt ttc ctc ctg gtg aaa atg aac acc cgg tca 317
Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys Met Asn Thr Arg Ser
45           50           55
```

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gtg acc acc atg gcg gtc att aac ttg gtg gtg gtc cac agc gtt ttt 365
Val Thr Thr Met Ala Val Ile Asn Leu Val Val Val His Ser Val Phe
60           65           70
```

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ctg ctg aca gtg cca ttt cgc ttg acc tac ctc atc aag aag act tgg 413
Leu Leu Thr Val Pro Phe Arg Leu Thr Tyr Leu Ile Lys Lys Thr Trp
75           80           85
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atg ttt ggg ctg ccc ttc tgc aaa ttt gtg agt gcc atg ctg cac atc 461
Met Phe Gly Leu Pro Phe Cys Lys Phe Val Ser Ala Met Leu His Ile
90           95           100          105
```

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cac atg tac ctc acg ttc cta ttc tat gtg gtg atc ctg gtc acc aga 509
His Met Tyr Leu Thr Phe Leu Phe Tyr Val Val Ile Leu Val Thr Arg
110          115          120
```

tac ctc atc ttc ttc aag tgc aaa gac aaa gtg gaa ttc tac aga aaa	557
Tyr Leu Ile Phe Phe Lys Cys Lys Asp Lys Val Glu Phe Tyr Arg Lys	
125 130 135	
ctg cat gct gtg gct gcc agt gct ggc atg tgg acg ctg gtg att gtc	605
Leu His Ala Val Ala Ala Ser Ala Gly Met Trp Thr Leu Val Ile Val	
140 145 150	
att gtg gta ccc ctg gtt gtc tcc cgg tat gga atc cat gag gaa tac	653
Ile Val Val Pro Leu Val Val Ser Arg Tyr Gly Ile His Glu Glu Tyr	
155 160 165	
aat gag gag cac tgt ttt aaa ttt cac aaa gag ctt gct tac aca tat	701
Asn Glu Glu His Cys Phe Lys Phe His Lys Glu Leu Ala Tyr Thr Tyr	
170 175 180 185	
gtg aaa atc atc aac tat atg ata gtc att ttt gtc ata gcc gtt gct	749
Val Lys Ile Ile Asn Tyr Met Ile Val Ile Phe Val Ile Ala Val Ala	
190 195 200	
gtg att ctg ttg gtc ttc cag gtc ttc atc att atg ttg atg gtg cag	797
Val Ile Leu Leu Val Phe Gln Val Phe Ile Ile Met Leu Met Val Gln	
205 210 215	
aag cta cgc cac tct tta cta tcc cac cag gag ttc tgg gct cag ctg	845
Lys Leu Arg His Ser Leu Leu Ser His Gln Glu Phe Trp Ala Gln Leu	
220 225 230	
aaa aac cta ttt ttt ata ggg gtc atc ctt gtt tgt ttc ctt ccc tac	893
Lys Asn Leu Phe Phe Ile Gly Val Ile Leu Val Cys Phe Leu Pro Tyr	
235 240 245	
cag ttc ttt agg atc tat tac ttg aat gtt gtg acg cat tcc aat gcc	941
Gln Phe Phe Arg Ile Tyr Tyr Leu Asn Val Val Thr His Ser Asn Ala	
250 255 260 265	
tgt agc agc aag gtt gca ttt tat aac gaa atc ttc ttg agt gta aca	989
Cys Ser Ser Lys Val Ala Phe Tyr Asn Glu Ile Phe Leu Ser Val Thr	
270 275 280	
gca att agc tgc tat gat ttg ctt ctc ttt gtc ttt ggg gga agc cat	1037
Ala Ile Ser Cys Tyr Asp Leu Leu Leu Phe Val Phe Gly Gly Ser His	
285 290 295	
tgg ttt aag caa aag ata att ggc tta tgg aat tgt gtt ttg tgc cgt	1085
Trp Phe Lys Gln Lys Ile Ile Gly Leu Trp Asn Cys Val Leu Cys Arg	
300 305 310	
tagccacaaa ctacagtatt catatttgct tcctttatat tgggaataaa atgggtatag	1145
gggaggtaag aatgggtattt cattacttga tcaaaaccat gccttgatgt acccaaaaaca	1205
aaaggactat aaaatgcaag agccctcatt gtagtcctta tgggatccct cccatctctg	1265
agtgatggcc gtacaaagac cagtgttggt gaatccacct ggagttgcaa tattacatta	1325
ttttccagta cagaatgtct gtgtggccca tgaaagcaac ataggtttta agagttttna	1385
gagtttcatt agctcattct aagttcctct gtttgaagca tggctctctta ggttttggac	1445
tgaactcaga cctttagttc ttttcatccc acttcaccat aggtaagtaa attctggcca	1505
ccaccagct ccaaagacac aaactctcct tcgctaacca ggttagatgt cccattcatc	1565
tcatgccctg ataaaaactg ataaggggag agaatagtta aaaatttttc tagggatatca	1625
taactctggt aggaagtcac ctgtctagac tcgagcaagc ttatgcatgc atgcggccg	1684
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<213> Homo sapiens	
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Asn Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr	

Leu	Thr	Tyr	Leu	Ile	Lys	Lys	Thr	Trp	Met	Phe	Gly	Leu	Pro	Phe	Cys	
				85					90					95		
aaa	ttt	gtg	agt	gcc	atg	ctg	cac	atc	cac	atg	tac	ctc	acg	ttc	cta	336
Lys	Phe	Val	Ser	Ala	Met	Leu	His	Ile	His	Met	Tyr	Leu	Thr	Phe	Leu	
			100					105				110				
ttc	tat	gtg	gtg	atc	ctg	gtc	acc	aga	tac	ctc	atc	ttc	ttc	aag	tgc	384
Phe	Tyr	Val	Val	Ile	Leu	Val	Thr	Arg	Tyr	Leu	Ile	Phe	Phe	Lys	Cys	
		115					120					125				
aaa	gac	aaa	gtg	gaa	ttc	tac	aga	aaa	ctg	cat	gct	gtg	gct	gcc	agt	432
Lys	Asp	Lys	Val	Glu	Phe	Tyr	Arg	Lys	Leu	His	Ala	Val	Ala	Ala	Ser	
	130					135					140					
gct	ggc	atg	tgg	acg	ctg	gtg	att	gtc	att	gtg	gta	ccc	ctg	gtt	gtc	480
Ala	Gly	Met	Trp	Thr	Leu	Val	Ile	Val	Ile	Val	Val	Pro	Leu	Val	Val	
145					150					155					160	
tcc	cgg	tat	gga	atc	cat	gag	gaa	tac	aat	gag	gag	cac	tgt	ttt	aaa	528
Ser	Arg	Tyr	Gly	Ile	His	Glu	Glu	Tyr	Asn	Glu	Glu	His	Cys	Phe	Lys	
				165				170						175		
ttt	cac	aaa	gag	ctt	gct	tac	aca	tat	gtg	aaa	atc	atc	aac	tat	atg	576
Phe	His	Lys	Glu	Leu	Ala	Tyr	Thr	Tyr	Val	Lys	Ile	Ile	Asn	Tyr	Met	
			180					185					190			
ata	gtc	att	ttt	gtc	ata	gcc	gtt	gct	gtg	att	ctg	ttg	gtc	ttc	cag	624
Ile	Val	Ile	Phe	Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Leu	Val	Phe	Gln	
		195					200					205				
gtc	ttc	atc	att	atg	ttg	atg	gtg	cag	aag	cta	cgc	cac	tct	tta	cta	672
Val	Phe	Ile	Ile	Met	Leu	Met	Val	Gln	Lys	Leu	Arg	His	Ser	Leu	Leu	
		210				215					220					
tcc	cac	cag	gag	ttc	tgg	gct	cag	ctg	aaa	aac	cta	ttt	ttt	ata	ggg	720
Ser	His	Gln	Glu	Phe	Trp	Ala	Gln	Leu	Lys	Asn	Leu	Phe	Phe	Ile	Gly	
					230				235						240	
gtc	atc	ctt	gtt	tgt	ttc	ctt	ccc	tac	cag	ttc	ttt	agg	atc	tat	tac	768
Val	Ile	Leu	Val	Cys	Phe	Leu	Pro	Tyr	Gln	Phe	Phe	Arg	Ile	Tyr	Tyr	
				245				250						255		
ttg	aat	gtt	gtg	acg	cat	tcc	aat	gcc	tgt	agc	agc	aag	gtt	gca	ttt	816
Leu	Asn	Val	Val	Thr	His	Ser	Asn	Ala	Cys	Ser	Ser	Lys	Val	Ala	Phe	
				260				265					270			
tat	aac	gaa	atc	ttc	ttg	agt	gta	aca	gca	att	agc	tgc	tat	gat	ttg	864
Tyr	Asn	Glu	Ile	Phe	Leu	Ser	Val	Thr	Ala	Ile	Ser	Cys	Tyr	Asp	Leu	
		275					280					285				
ctt	ctc	ttt	gtc	ttt	ggg	gga	agc	cat	tgg	ttt	aag	caa	aag	ata	att	912
Leu	Leu	Phe	Val	Phe	Gly	Gly	Ser	His	Trp	Phe	Lys	Gln	Lys	Ile	Ile	
		290				295					300					
ggc	tta	tgg	aat	tgt	gtt	ttg	tgc	cgt								939
Gly	Leu	Trp	Asn	Cys	Val	Leu	Cys	Arg								
					310											

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 Asn Asp Phe Met Ser Gly Phe Leu Cys Phe Ser Ile Asn Val Arg Ala
 20 25 30

Phe Gly Ile Thr Val Pro Thr Pro Leu Tyr Ser Leu Val Phe Ile Ile
 35 40 45
 Gly Val Ile Gly His Val Leu Val Val Leu Val Leu Ile Gln His Lys
 50 55 60
 Arg Leu Arg Asn Met Thr Ser Ile Tyr Leu Phe Asn Leu Ala Ile Ser
 65 70 75 80
 Asp Leu Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met
 85 90 95
 Lys Gly Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly
 100 105
 Phe Tyr Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu
 115 120 125
 Thr Ile Asp Arg Tyr Leu Ala Val Val His Val Val Phe Ala Leu Arg
 130 135 140
 Ala Arg Thr Val Thr Phe Gly Ile Ile Ser Ser Ile Ile Thr Trp Val
 145 150 155 160
 Leu Ala Ala Leu Val Ser Ile Pro Cys Leu Tyr Val Phe Lys Ser Gln
 165 170 175
 Met Glu Phe Thr Tyr His Thr Cys Arg Ala Ile Leu Pro Arg Lys Ser
 180 185 190
 Leu Ile Arg Phe Leu Arg Phe Gln Ala Leu Thr Met Asn Ile Leu Gly
 195 200 205
 Leu Ile Leu Pro Leu Leu Ala Met Ile Ile Cys Tyr Thr Arg Ile Ile
 210 215 220
 Asn Val Leu His Arg Arg Pro Asn Lys Lys Lys Ala Lys Val Met Arg
 225 230 235 240
 Leu Ile Phe Val Ile Thr Leu Leu Phe Phe Leu Leu Leu Ala Pro Tyr
 245 250 255
 Tyr Leu Ala Ala Phe Val Ser Ala Phe Glu Asp Val Leu Phe Thr Pro
 260 265 270
 Ser Cys Leu Arg Ser Gln Gln Val Asp Leu Ser Leu Met Ile Thr Glu
 275 280 285
 Ala Leu Ala Tyr Thr His Cys Cys Val Asn Pro Val Ile Tyr Val Phe
 290 295 300
 Val Gly Lys Arg Phe Arg Lys Tyr Leu Trp Gln Leu Phe Arg Arg His
 305 310 315 320
 Thr Ala Ile Thr Leu Pro Gln Trp Leu Pro Phe Leu Ser Glu Asp Arg
 325 330 335
 Ala Gln Arg Ala Ser Ala Arg Leu Pro Ser Thr Val Glu Ile Glu Thr
 340 345 350
 Ser Ala Asp Leu
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<210> 5
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 <212> PRT
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<400> 5
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 1 5 10 15
 Val Phe Leu Ser Thr Leu Pro Phe Trp Val Asp Tyr Ile Met Lys Gly
 20 25 30
 Asp Trp Ile Phe Gly Asn Ala Met Cys Lys Phe Val Ser Gly Phe Tyr
 35 40 45
 Tyr Leu Gly Leu Tyr Ser Asp Met Phe Phe Ile Thr Leu Leu Thr Ile
 50 55 60
 Asp Arg Tyr Leu
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<210> 6
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus

<221> VARIANT

<222> (1)...(1)
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 L or I or V or M or F or Y or W or C

<221> VARIANT
 <222> (2)...(2)
 <223> Xaa at position 2 can be G or S or T or A or
 N or P or D or E

<221> VARIANT
 <222> (3)...(3)
 <223> Xaa at position 3 can not be E or D or
 P or K or R or H

<221> VARIANT
 <222> (4)...(4)
 <223> Xaa at position 4 can
 be any amino acid

<221> VARIANT
 <222> (5)...(5)
 <223> Xaa at position 5 can
 be any amino acid

<221> VARIANT
 <222> (6)...(6)
 <223> Xaa at position 6 can be L or I or V or M or
 N or Q or G or A

<221> VARIANT
 <222> (7)...(7)
 <223> Xaa at position 7 can
 be any amino acid

<221> VARIANT
 <222> (8)...(8)
 <223> Xaa at position 8 can
 be any amino acid

<221> VARIANT
 <222> (9)...(9)
 <223> Xaa at position 9 can be L or I or V or M or
 F or T

<221> VARIANT
 <222> (10)...(10)
 <223> Xaa at position 10 can be G or S or T or A or
 N or C

<221> VARIANT
 <222> (11)...(11)
 <223> Xaa at position 11 can be L or I or V or M
 or F or Y or W or S or T or A or C

<221> VARIANT
 <222> (12)...(12)
 <223> Xaa at position 12 can be D or E or N or H

<221> VARIANT
 <222> (14)...(14)
 <223> Xaa at position 14 can be F or Y or W or C
 or S or H

<221> VARIANT
 <222> (15)...(15)
 <223> Xaa at position 15
 can be any amino acid

<221> VARIANT
<222> (16)...(16)
<223> Xaa at position 16
can be any amino acid

<221> VARIANT
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Xaa